

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: November 8, 2001, 13:04:36 ; Search time 5356.8 seconds  
(without alignments)  
17812.975 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169  
Sequence: 1 aatcttgctcagttactctc.....cttggtccctccatgtcag 6169

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 8

Total number of hits satisfying chosen parameters: 2551636

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:

1: gb\_ba1:\*  
2: gb\_ba2:\*  
3: gb\_ba3:\*  
4: gb\_in1:\*  
5: gb\_in2:\*  
6: gb\_in3:\*  
7: gb\_om:\*  
8: gb\_ov:\*  
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13: gb\_pl2:\*  
14: gb\_pl3:\*  
15: gb\_pl4:\*  
16: em\_ba1:\*  
17: em\_ba2:\*  
18: em\_fun:\*  
19: em\_htgo\_hum:\*  
20: em\_htgo\_inv:\*  
21: em\_htgo\_rnd:\*  
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32: em\_htg\_other:\*  
33: em\_htg\_rnd:\*  
34: em\_hum1:\*  
35: em\_hum2:\*  
36: em\_hum3:\*  
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43: em\_or:\*

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46: em\_ph:\*  
47: em\_pl:\*  
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49: em\_sts:\*  
50: em\_sy:\*  
51: em\_un:\*  
52: em\_v1:\*  
53: gb\_sts1:\*  
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92: gb\_pr8:\*  
93: gb\_pr9:\*  
94: gb\_rn1:\*  
95: gb\_rn2:\*  
96: gb\_in4:\*  
97: gb\_pr10:\*  
98: em\_ba3:\*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5552	90.0	79376	92 HS454G6	298750 Human DNA s
2	5300	85.9	5300	88 AF007562	AF007562 Homo sapi
3	5243	85.0	170425	68 AC024490	AC024490 Homo sapi
4	2285	37.0	2800	93 HSMYOC1	AF048791 Homo sapi
5	1035	16.8	1086	93 HSGIC1A1	Z57171 Homo sapien
6	978	15.9	1228	85 AB006686S1	AB006686 Homo sapi
7	647	10.5	1934	91 D88214	D88214 Homo sapien
8	640	10.4	1871	9 AX004457	AX004457 Sequence

9	640	10.4	1871	9	AX004474	AX004474 Sequence
10	640	10.4	1999	9	AR030962	AR030962 Sequence
11	640	10.4	1999	9	AR066022	AR066022 Sequence
12	640	10.4	1999	9	AR069089	AR069089 Sequence
13	640	10.4	2000	97	HSU85257	HSU85257 Human trabe
14	640	10.4	2002	9	AB4847	AB4847 Sequence 2
15	626	10.1	2001	93	HSAF001620	HSAF001620 Homo sapi
16	604	9.8	1512	9	AB4848	AB4848 Sequence 3
17	604	9.8	1512	9	AR030963	AR030963 Sequence
18	604	9.8	1512	9	AR066023	AR066023 Sequence
19	604	9.8	1512	9	AR069090	AR069090 Sequence
20	594	9.6	2000	9	AB4850	AB4850 Sequence 2
21	558	9.0	1512	9	AB4851	AB4851 Sequence 3
22	366	5.9	1969	9	AR020502	AR020502 Sequence
23	366	5.9	1969	10	I36470	I36470 Sequence 2
24	330	5.3	1491	9	AR020503	AR020503 Sequence
25	330	5.3	1491	10	I36471	I36471 Sequence 3
26	189	3.1	228	88	AF007564	AF007564 Homo sapi
27	74	1.2	49868	78	AC090368	AC090368 Homo sapi
28	74	1.2	73431	82	AP000575	AP000575 Homo sapi
29	74	1.2	109290	84	HS838L14	HS838L14 Homo sapi
30	74	1.2	157454	82	AP001462	AP001462 Homo sapi
31	74	1.2	166269	82	AP001187	AP001187 Homo sapi
32	74	1.2	171980	82	AP000928	AP000928 Homo sapi
33	74	1.2	176653	82	AP001857	AP001857 Homo sapi
34	74	1.2	178100	82	AP001558	AP001558 Homo sapi
35	74	1.2	203300	85	AC000134	AC000134 Homo sapi
36	72	1.1	200422	73	AC068553	AC068553 Homo sapi
37	70	1.1	153831	75	AC079168	AC079168 Homo sapi
38	70	1.1	199937	86	AC007055	AC007055 Homo sapi
39	65	1.1	111107	86	AC005924	AC005924 Homo sapi
40	65	1.1	164945	68	AC024251	AC024251 Homo sapi
41	65	1.1	175336	83	CNS01D7Q	AL132838 Homo sapi
42	64	1.0	136886	89	AL138889	Human DNA
43	64	1.0	168210	87	AC018719	Homo sapi
44	64	1.0	168544	89	AL133344	Human DNA
45	64	1.0	179040	67	AC022732	Homo sapi

## ALIGNMENTS

RESULT 1	HS454G6/c	79376 bp	DNA	PRI	23-NOV-1999
LOCUS	Human DNA sequence from PAC 454G6 on chromosome 1q24. Contains				
DEFINITION	trabecular meshwork inducible glucocorticoid response protein,				
	TIGR, myocillin, ESTs and STS.				
ACCESSION	Z98750				
VERSION	Z98750.1	GI:2887277			
KEYWORDS	1q24; myocillin; TIGR.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 79376)				
AUTHORS	Deadman,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (27-OCT-1997) Chromosome 1 Project Group				
	(http://www.sanger.ac.uk/HGP/Chr1/) Sanger Centre, Hinxton,				
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:				
	humuery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk				
	On Feb 14, 1998 this sequence version replaced gi:2465060.				
	IMPORTANT: This sequence is not the entire insert of clone 454G6.				
	It may be shorter because we only sequence overlapping sections				
	once, or longer because we arrange for a small overlap between				
	neighbouring submissions.				
	During sequence assembly data is compared from overlapping clones.				
	Where differences are found these are annotated as variations				
	together with a note of the overlapping clone name. Note that the				
	variations annotated may not be found in the sequence submission				
	corresponding to the overlapping clone as we submit sequences with				
	only a small overlap as described above.				

## FEATURES

source	This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre chromosome 1 mapping group. Further information can be found at <a href="http://www.sanger.ac.uk/HGP/Chr1/">http://www.sanger.ac.uk/HGP/Chr1/</a>
	This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.
	The true left end of clone 454G6 is at 1 in this sequence. The true left end of clone 560B9 is at 79273.
	454G6 is from the library RPC13 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.
	For further details see <a href="http://bacpac.med.buffalo.edu/">http://bacpac.med.buffalo.edu/</a> .
	Location/Qualifiers
	1..79376
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	/db_xref="taxon:9606"
	/chromosome="1"
	/map="1q24"
	/clone="RP3-454G6"
	/clone.lib="RPC1-3"
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	/note="19 copies of 2 mer 82 & conserved"
prim_transcript	1914..>3968
	/note="match: multiple ESTs
	match: R56676 AA043968 W63639 F12081 AA046699
	match: F02925 AA043968 W00634 R36066 AA13383
	match: AA163561 F02925 AA133540 W00634 R36066
	match: AA13383 AA163561 N89173 AA174814 AA057059
	match: AA329084 W47082 AA043955 AA341783 AA333681
	match: AA046487 AA369741 H08313 AA186895 H32730
	match: H08333 H08236 N42052 D61944 R27102 N32353
	match: N30491 AA307150 AA192"
repeat_region	3703..3746
	/note="22 copies of 2 mer 89 & conserved"
repeat_region	4051..4183
	/note="AluSq repeat: matches 1..133 of consensus
	incomplete repeat"
repeat_region	4200..4502
	/note="AluSq repeat: matches 2..301 of consensus"
	4659..4851
	/note="AluSx repeat: matches 2..194 of consensus
	incomplete repeat"
repeat_region	5216..5345
	/note="AluDo repeat: matches 132..1 of consensus
	incomplete repeat"
repeat_region	7759..7907
	/note="MIR repeat: matches 174..1 of consensus"
repeat_region	7933..9328
	/note="TIGER1 repeat: matches 1..1472 of consensus"
	9332..9626
	/note="AluSg repeat: matches 1..289 of consensus"
	9639..10335
	/note="TIGER1 repeat: matches 1469..2174 of consensus"
	10343..10642
	/note="AluSg repeat: matches 1..300 of consensus"
repeat_region	10643..10856
	/note="TIGER1 repeat: matches 2175..2417 of consensus"
	<10903..>16855
	/note="endogenous retroviral sequence"
	10949..11384
	/note="LRR2 repeat: matches 31..449 of consensus"
misc_feature	15835..15870
	/note="18 copies of 2 mer 83 & conserved"
repeat_region	16856..17286
	/note="LRR2 repeat: matches 31..449 of consensus"
repeat_region	17287..17574
	/note="AluSg repeat: matches 15..300 of consensus"
repeat_region	18294..18650
	/note="THE1B repeat: matches 338..1 of consensus"
repeat_region	18877..19180



QY 661 agtgaatgaagcagltgaacatgttcgacaacccctcccgctctataccagggaacacaaa 720  
|||||  
Db 67746 AGGATATTAGCCAGATTGACCATGTTCCGACACACCTCCCGCTATTACAGAGGAACACAAA 67687  
QY 721 attgacatggcctgaagccttgacattctcaagggaatgatgaaaaacttgaggaacaaa 780  
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Db 67686 ATTGATGGGCTTAAGCCTGATCTTCAAGGGAAATATGAAAACCTGAGACCAAAACAAA 67627  
QY 781 gacatggtltaaaaggcaacagacatgtgagccttcaaggcagatgcccctcagca 840  
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Db 67626 GACATGGTTAAAAGGACACAGAACATGTGAGCTTTCAAGACAGCAGTCCCTCAGCA 67567  
QY 841 gggaaccctgaggcaattgaccttaaggaaagccagtttcttlaaggaaacttlaaggaaatc 900  
Db 67566 GGGAACCTGAGGATTTGCCCTTAGAAGAGCCAGTTTCTTAAGGAATCTTAAGAAATC 67507  
QY 901 tgaagaagatcaatgaatttlaacaaattlaagtaaaacaataatgcataatcag 960  
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Db 67506 TTGAAAGATCATGAAATTTAAACCATTTTAAAGTAAATAAATAATGGAATGATTAATCAG 67447  
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Db 67446 TTTAGACATGGGTCCCAATTTTAAAGTCAGGCATACAGATTAACGTGTCCAGCTCC 67387  
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Dp	65526	TGCAGAGCGTCGAAACCTTGGAATCAGAGACGTGGTTTTTCTTTGCGGTTCTGCGAATT	65467
Qy	2941	ggttcgctgtcgacgcgttgggcaagtgctctctctctcccttgggcaatgctctctgct	3000
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Dp	65406	ATTAAGACCTTTGCAAGCTCTCTGTTCTGTGAACACTTCCCTGATATCTCTGTAGGGG	65347
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Qy	3121	ggaacgaaggaagcaggaagcctgggtgtctccatagctccactcaatcaatcagtcagacatc	3180
Dp	65286	GGACAGGAAGGACGACAGACGTGGGTGCTCCATCAGTCTCTCAGTACCTCAGACATC	65227
Qy	3181	caggaecgaagcaacatgctctcaagaaagctcaatgaacccaacagcacatcttccct	3240
Dp	65226	CAGGACCGAGAGCCCAATGCTTTAGGAAGCTCAATGMACCCAACAGCCATTTTCTCT	65167
Qy	3241	tcccaagaatagaaataggcaatgttcgaataatcaaaaaaagatgcagagtaactgtgt	3300
Dp	65166	TCCCTTAACCATTAAGCAATGGCAATTTGGCCAAATTAACCAAAAAGATCAGAGCAATCTGGT	65107
Qy	3301	ggtacgctctgccttgaccaatcgaaaactgggcagagcagctggaataatgcagaagatgt	3360
Dp	65106	GGTACTTTTGGCTGTGGCAATTCAAAACGTGGCCACAGCAAGTGGAAATGCCAGAGATTG	65047
Qy	3361	ttaaactttcaaccttgaccagacacccaacgcagctcagcagtgacgtctgcagcaacg	3420
Dp	65046	TTTAACTTTTCCCTGTGACCAACACACCCACGCAAGCTCAGCACTGTGACACACAGG	64987
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Qy	3601	cctgtattctaaatactataatcttccctctacaagctgagtaactctgagcaatcaaga	3660
Dp	64806	CTGTATTTCTTAATACTATAATTTTCTTTTACAAAGCTGAATTAATCTGACCAAGTCAAG	64747
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ACCESSION AF007562
VERSION 1
KEYWORDS protein (TIGR) gene, promoter region and partial mRNA sequence.
SOURCE AF007562.1 GI:2970123
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 5300)
Nuyen,T.D., Chen,P., Huang,W.D., Chen,H., Johnson,D. and
Polansky,J.R.
Gene structure and properties of TIGR, an olfactomedin-related
glycoprotein cloned from glucocorticoid-induced trabecular meshwork
cells
JOURNAL J. Biol. Chem. 273 (11), 6341-6350 (1998)
MEDLINE 98165818
REFERENCE 2 (bases 1 to 5300)
Nuyen,T.D., Chen,P., Chen,H. and Polansky,J.R.
Direct Submission
JOURNAL Submitted (10-JUN-1997) Ophthalmology, University of California San
Francisco, 10 Kirham Street, San Francisco, CA 94143-0730, USA
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* 56897 62860: contig of 5964 bp in length
* 62861 62960: gap of 100 bp
* 62961 72552: contig of 9592 bp in length
* 72553 72652: gap of 100 bp
* 72653 83310: contig of 10658 bp in length
* 83311 83410: gap of 100 bp
* 83411 92992: contig of 9582 bp in length
* 92993 93092: gap of 100 bp
* 93093 103986: contig of 10794 bp in length
* 103987 119418: contig of 15432 bp in length
* 119419 119518: gap of 100 bp
* 119519 136695: contig of 17177 bp in length
* 136696 136795: gap of 100 bp
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REFERENCE	AUTHORS	TITLE	ORGANISM	SEGMENT	KEYWORDS	VERSION	ACCESSION	LOCUS	LOCUS DEFINITION	RESULT 4
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QY	5616	tcacctgagaaagccctcccaacaaatgaccttgaacctgaagccagctgtcagagcccaagaaagc								
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QY	5676	caggagagggctctcagagagagctgtggcacccctgagaccgtgagagcggagagcagctgtgaaac								
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QY	5856	agccagagaggtatgacaaaggtctgagaagaagggccagtgctcccaagaccgagacaactgtctgg								
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 VERSION 297171.1 GI:2425156  
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 REFERENCE 1 (bases 1 to 1086)  
 Stone, E.M., Pingert, J.H., Alvard, W.L., Nguyen, T.D., Polansky, J.R., Sundin, S.L., Nishimura, D., Clark, A.F., Nystuen, A., Nichols, B.E., Ritch, R., Kalenak, J.W., Craven, E.R. and Sheffield, V.C.  
 Identification of a gene that causes primary open angle glaucoma Science 275 (5300), 668-670 (1997)  
 TITLE JOURNAL MEDLINE 97158493  
 REFERENCE 2 (bases 1 to 1086)  
 Adam, M.F., Belmouden, A., Binstli, P., Brezin, A.P., Valton, F., Becheville, A., Dascombe, J.C., Copin, B., Gomez, L., Chaventre, A., Bach, J.F. and Garçon, H.J.  
 Recurrent mutations in a single exon encoding the evolutionarily conserved olfactomedin-homology domain of TRK in familial open-angle glaucoma Hum. Mol. Genet. 6 (12), 2091-2097 (1997)

JOURNAL









MoBuyoshi Shimizu, Keio University School of Medicine, Department of Molecular Biology; 35 Shinanomachi, Shinjuku-ku, Tokyo 160, Japan (E-mail:shimizu@med.keio.ac.jp, Tel:03-3351-2370, Fax:03-3351-2370)

2 (sites)

REFERENCE  
Kubota, R., Noda, S., Wang, Y., Minoshima, S., Asakawa, S., Kudoh, J., Meshima, Y., Oguchi, Y. and Shimizu, N.  
A novel myosin-like protein (myocilin) expressed in the connecting cilium of the photoreceptor: molecular cloning, tissue expression, and chromosomal mapping  
Genomics 41 (3), 360-369 (1997)

JOURNAL  
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VERSION AX004457.1 GI:927916  
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AUTHORS Anctil, J. L. and Cote, G.  
TITLE Molecular diagnosis of glaucomas associated with chromosomes 1,  
and method of treatment thereof  
JOURNAL Patent: WO 9916898-A 1 08-APR-1999;  
ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)  
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	Mammalia; Eutheria; Primates; Catarrhini; Homini; Homo.		
REFERENCE	1 (bases 1 to 1871)		
AUTHORS	Anctil,J.L., and Cote,G.		
TITLE	Molecular diagnosis of glaucomas associated with chromosomes 1,		
JOURNAL	and method of treatment thereof		
	Patent: WO 9916898-A 18 08-Apr-1999;		
	ANCTIL JEAN LOUIS (CA); COTE GILLES (CA)		
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Query Match	10.4%	Score 640;	DB 9;	Length 1871;
Best Local Similarity	100.0%;	Pred. No. 0;		
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Qy 5481 tatacctcagctgtgagcagctcccaatgaaatccagctgcccagagagccaaagcagtg 5540
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LOCUS AR066022 1999 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5849879.
ACCESSION AR066022
VERSION AR066022.1 GI:5996238
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE Methods for the diagnosis of glaucoma
JOURNAL Patent: US 5849879-A 2 15-Dec-1998;
FEATURES
source 1. 1999
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%: Score 640; DB 9; Length 1999;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 2 from patent US 5854415.
ACCESSION AR069089
VERSION AR069089.1 GI:6001296
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1999)
AUTHORS Nguyen,T.D., Polansky,J.R. and Huang,W.
TITLE Methods for the diagnosis of glaucoma
JOURNAL Patent: US 5854415-A 2 29-Dec-1998;
FEATURES
source 1. 1999
BASE COUNT 537 a 508 c 534 g 420 t
ORIGIN

Query Match 10.4%: Score 640; DB 9; Length 1999;
Best Local Similarity 100.0%: Pred. No. 0;
Matches 640; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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ACCESSION AB4847  
VERSION AB4847.1 GI:6733711  
KEYWORDS  
SOURCE unidentified.  
ORGANISM unidentified.  
REFERENCE 1 (bases 1 to 2002)  
AUTHORS Huang, W. and Nguyen, T.D.  
TITLE DIAGNOSIS AND PROGNOSIS OF GLAUCOMA  
JOURNAL Patent: WO 9844108-A 2 08-OCT-1998;  
HUANG WEIDONG (US); NGUYEN THAI D (US)  
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DEFINITION Homo sapiens trabecular meshwork-induced glucocorticoid response protein (TIGR) mRNA, complete cds.  
ACCESSION AF001620  
VERSION AF001620.1 GI:2104788  
KEYWORDS  
SOURCE human.  
ORGANISM human.

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 2061)  
AUTHORS Escribano, J., Ortego, J. and Coca-Prados, M.  
TITLE Isolation and characterization of cell-specific cDNA clones from a subtractive library of the ocular ciliary body of a single normal human donor: transcription and synthesis of plasma proteins  
J. Biochem. 118 (5), 921-931 (1995)  
JOURNAL MEDLINE  
REFERENCE 2 (bases 1 to 2061)  
AUTHORS Stone, E.M., Finger, J.H., Alward, W.L.M., Nguyen, T.D., Polansky, J.R., Sundén, S.L.F., Nishimura, D., Clark, A.F., Nystuen, A., Nichols, B.E., Mackey, D.A., Ritch, R., Kalenak, J.W., Craven, E.R. and Sheffield, V.C.  
TITLE Identification of a gene that causes primary open angle glaucoma  
Science 275 (5300), 668-670 (1997)  
JOURNAL MEDLINE  
REFERENCE 3 (bases 1 to 2061)  
AUTHORS Ortego, J., Escribano, J. and Coca-Prados, M.  
TITLE Cloning and characterization of subtracted cDNAs from a human ciliary body library encoding TIGR, a protein involved in juvenile open angle glaucoma with homology to myosin and olfactomedin  
FEBS Lett. 413 (2), 349-353 (1997)  
JOURNAL MEDLINE  
REFERENCE 4 (bases 1 to 2061)  
AUTHORS Coca-Prados, M., Ortego, J. and Escribano, J.  
TITLE Direct Submission  
Submitted (29-APR-1997) Ophthalmology and Visual Science, Yale University School of Medicine, 330 Cedar St, New Haven, CT 06520, USA  
JOURNAL MEDLINE  
REFERENCE 1. 2061  
Location/Qualifiers

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Best Local Similarity 100.0% Pred. No. 0;

Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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